

RAW SEQUENCE LISTING

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Application Serial Number: 10/559, 415
Source: JFWP
Date Processed by STIC: 12/16/2005

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IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/559,415

DATE: 12/16/2005

TIME: 15:14:37

Input Set : A:\Stripped Sequence Listing.txt
 Output Set: N:\CRF4\12162005\J559415.raw

3 <110> APPLICANT: AstraZeneca AB et al
 5 <120> TITLE OF INVENTION: Diagnostic Method
 7 <130> FILE REFERENCE: 101073-1P WO
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/559,415
 C--> 10 <141> CURRENT FILING DATE: 2005-12-06
 12 <150> PRIOR APPLICATION NUMBER: 0313081.2
 13 <151> PRIOR FILING DATE: 2003-06-06
 15 <160> NUMBER OF SEQ ID NOS: 191
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 7430
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
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 29 gcgggagcgc tcagtccccgg cgagcggcgg cagctggacg aggaggcggg aggcggccaag 180
 31 gcgaggactgc tgctcaagct gctcttggcc aaggaggcggg accacttcca ggacactgcgg 240
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 35 gggccgcccga agcccgccga aggcgcgggt tctacctaca gcgtcctgta caccatgcc 360
 37 tcagactcag aaagcagcag ctcctcagc agtgtggca ctaccggaa ggcggcgtcc 420
 39 ccaccacccc tcctcaactga ccagcaagtg aatgagaagg tggagaacct ctccattcag 480
 41 ctgcggctga tgacccggga gagaaaacgag ctccgcaagc gcctggcctt tgctacgcat 540
 43 ggcacggcct ttgacaagag gccttaccac aggctgaatc ctgactatga gaggtgtaag 600
 45 atccagtgcg tgcgagccat gtcggacctg cagaggctgc agaaccagca caccacgc 660
 47 ttgaagaggt gtgaggaggt ggcacaaggag actgacttct accacacact ccacagccgg 720
 49 ctccctgagtg accagactcg gctgaaggat gacgtggaca tgctgaggcg ggagaatggg 780
 51 cagctgctgc gggagcgaaa cctgctcagc cagtcatggg aggacatgaa gcggctccac 840
 53 gaggaggacc agaaggagat cgtgacccctc cgtgcccagc agcagcaggt gttgaagcac 900
 55 aacgggtcat ccgagattct caacaaactg tatgacacgg ccatggacaa gttggaggtg 960
 57 gtcaagaagg actatgacgc cttcggaag aggtacagtg agaaaagtgc catccacaat 1020
 59 gcagaccta gccccttga gcagctgggg gaggagaacc agcggttgtc gaaggac 1080
 61 gagatgctga cccagcagag ggacacggcc atccagctgc agcaccagtg cgcctctcc 1140
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 65 ctgcagtggg agatggagct gctgcagtca gagctgaccg agctgagaac cacgcagggt 1260
 67 aagacagcaa aggagtccga gaaatacagg gaggagcggg acgctgtgtc cagcgagtac 1320
 69 aagctcatca tgagttagcg tgaccaggctc atctctgagc tggacaagct gcagaccgaa 1380
 71 gtggagctgg ccgagttccaa gctcaagagc agcacatctg agaagaaggc ggccaatgag 1440
 73 gagatggagg cgctcgccga gatcaaagac acggtgacaa tggatgctgg gagagccaa 1500
 75 aaggaggttg aaatccctcg aaagcagtgc aaggctctgt gccaggagct gaaggaagcc 1560
 77 ctccaggagg cggatgtggc caagtgccgg cgggactggg cttccagga gcgagacaag 1620
 79 atttagcag agcgtgacag catccggaca ctgtgtgaca acctgaggcg ggagcgggac 1680
 81 cgtcggtga gcgagctggc tgaggccctg cgcagccctgg atgacaccccg caagcagaag 1740

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85	gaggccccgt	tccgacagct	gatggcccac	agctcccacg	actcggccat	tgacacggat	1860
87	tccatggagt	gggaaacgga	agttgttagag	ttcgagaggg	agacggagga	tattgacttg	1920
89	aaggcactgg	ggtttgatat	ggcagaaggt	gtgaatgagc	cttgtttccc	ggggactgt	1980
91	ggcatatttg	tcactaaagt	ggacaaagga	agcattgctg	atggccgctt	aagggtcaat	2040
93	gactggctgc	tgagaatcaa	cgtgtggac	ctcatcaaca	aggacaagaa	gcagccatc	2100
95	aaggcgctcc	tcaatggga	ggggggccatc	aacatggtcg	tgccggcggag	gaagtccctg	2160
97	ggtggaaagg	tggtcacgcc	gctgcacatc	aacctcagtg	gacagaaaaga	cagtggcatc	2220
99	agtcctggaga	atggagtgt	tgctgcccgt	gtgctgcctg	gaagccctgc	cgctaaagaa	2280
101	gggtcccttg	ctgtggaga	caggatcggt	gcgtatcaatg	gcattgcact	ggacaacaag	2340
103	tctctgaatg	aatgtgaatc	tctgtgcgg	agctgccagg	actccctgac	cctgtccctc	2400
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107	gactctgata	agatgctgag	ttttcgagcc	catggcccgg	aggtccaggg	tcataacaaa	2520
109	cggaacttga	tacagcacaa	taactccacg	cagacagaca	tcttctacac	ggacaggctg	2580
111	gaagacagga	aggagccagg	cccccccagga	ggcagcagct	cctttctgca	taagccattc	2640
113	cctgggggac	ccttgcagg	ctgccccca	gcctgtccca	gtgcctctga	gcgtagcctg	2700
115	agtccttc	gctcagatgc	ctctgggac	cgtgctttg	ggctgggtgg	cgtgcgtggc	2760
117	cggcggccac	tgctccctt	tgagaccgag	gtggccccc	gtgggggtgg	ggaggcctcc	2820
119	ctggacaagg	cagactctga	aggctccaa	agcggcggga	cctggccaa	ggccatgctc	2880
121	agtcacgg	cagtgcctga	gaagctctct	gtttataaaa	agccaaagca	aaaaagtcc	2940
123	atcttgacc	ctaacactt	caaacgcccc	cagacacccc	ccaaaataga	ctacctgctt	3000
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127	ccaaaacctc	ccagaaggag	cgactccatt	aagtccagc	acaggctgga	gactagctcc	3120
129	gagtcaag	ccactcttgt	gggcagctcc	ccatccacta	gtccccccag	cgcctgccc	3180
131	cctgacgtgg	accccgggga	gcccatgcac	gcatcacccc	ctcgcaaggc	cagggtccgc	3240
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135	tcctgtgatg	aggacctcac	ctcccagaag	gtggatgagc	tggggcagaa	gcgtgcgg	3360
137	ccaaaatctg	ctcccagtt	tcggccgaag	cttgcctccag	tagtGattcc	tgctcagttc	3420
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141	gcaccttact	cgcctggca	ttccagccgg	cacagcaacc	ccccgtata	ccctagcagg	3540
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145	cgaacccca	tctacactgt	gcgcagtcac	agggtcgccc	cctgcagctc	tccacctgcg	3660
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151	aactcaactgc	cctccagcgc	ccgcctgggt	tcttcagta	acttgcagtt	caaggcggaa	3840
153	cgcattaaaa	tcccatcaac	accaagat	ccggggagtg	tcgtgggctc	cgagagaggt	3900
155	tcagtgtcac	attctgaatg	cagca	ccacgtcac	ccctgaacat	cgacaccc	3960
157	tcctcttgta	gccagtc	gacctcagcc	tccacattgc	ccagaatcgc	tgtcaacccc	4020
159	gctccctcg	gggagcggag	aaaggacagg	ccttatgtgg	aggagccacg	ccacgtgaag	4080
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165	cagttactgg	agttcaacgg	cataaacctg	cgagcgcac	cgagcagca	ggcgcggc	4260
167	atcatcgccc	agcagtgtga	taccatcacc	atcctggccc	agtacaaccc	ccacgtgcac	4320
169	cagctcagca	gccactccc	gtccagctca	cac	ctggcgtac	ccactccact	4380
171	ctccaggggca	gtggcaccac	caccccgag	catccatctg	tcatcgaccc	actgatggag	4440
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187	agcttaaga	aggacgacat	cctctacgtg	gatgacacct	taccccaggg	cacgttcggg	4920
189	tcctggatgg	cttggcagct	ggacgagaat	gcccagaaga	tccagcgcgg	gcagattccc	4980
191	agcaaataatg	tgtatggacca	agaattctcc	aggaggctca	gcatgtctga	agtc当地agat	5040
193	gacaatagcg	ccacaaaagac	gctgtcagcg	gctgcacgcc	ggtcctttt	tcggaggaaa	5100
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227	tgtatcgaga	tgtctcaaaag	agaacccccc	ggatcactcg	tttacaagcc	ttttctaagt	6120
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263	ttgttcaaaa	aagagacaag	tttcagtcct	caatgtgc	cttgcgtt	cagtgacaa	7200
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267	accctctggg	ggtagggct	ttttctaaag	ttacaggcag	agtgggactg	agatggtaca	7320
269	gtgtgcacag	acaggtactg	agctgacaga	ctgggatttt	ctgtactaaa	atgttacttt	7380
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277 <213> ORGANISM: Homo sapiens
 279 <400> SEQUENCE: 2
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 286 20 25 30
 289 Ala Gly Ala Leu Ser Pro Gly Glu Arg Arg Gln Leu Asp Glu Glu Ala
 290 35 40 45
 293 Gly Gly Ala Lys Ala Glu Leu Leu Leu Lys Leu Leu Ala Lys Glu
 294 50 55 60
 297 Arg Asp His Phe Gln Asp Leu Arg Ala Ala Leu Glu Lys Thr Gln Pro
 298 65 70 75 80
 301 His Leu Leu Pro Ile Leu Tyr Leu Asn Gly Val Val Gly Pro Pro Gln
 302 85 90 95
 305 Pro Ala Glu Gly Ala Gly Ser Thr Tyr Ser Val Leu Ser Thr Met Pro
 306 100 105 110
 309 Ser Asp Ser Glu Ser Ser Ser Leu Ser Ser Val Gly Thr Thr Gly
 310 115 120 125
 313 Lys Ala Pro Ser Pro Pro Pro Leu Leu Thr Asp Gln Gln Val Asn Glu
 314 130 135 140
 317 Lys Val Glu Asn Leu Ser Ile Gln Leu Arg Leu Met Thr Arg Glu Arg
 318 145 150 155 160
 321 Asn Glu Leu Arg Lys Arg Leu Ala Phe Ala Thr His Gly Thr Ala Phe
 322 165 170 175
 325 Asp Lys Arg Pro Tyr His Arg Leu Asn Pro Asp Tyr Glu Arg Leu Lys
 326 180 185 190
 329 Ile Gln Cys Val Arg Ala Met Ser Asp Leu Gln Ser Leu Gln Asn Gln
 330 195 200 205
 333 His Thr Asn Ala Leu Lys Arg Cys Glu Glu Val Ala Lys Glu Thr Asp
 334 210 215 220
 337 Phe Tyr His Thr Leu His Ser Arg Leu Leu Ser Asp Gln Thr Arg Leu
 338 225 230 235 240
 341 Lys Asp Asp Val Asp Met Leu Arg Arg Glu Asn Gly Gln Leu Leu Arg
 342 245 250 255
 345 Glu Arg Asn Leu Leu Gln Gln Ser Trp Glu Asp Met Lys Arg Leu His
 346 260 265 270
 349 Glu Glu Asp Gln Lys Glu Ile Gly Asp Leu Arg Ala Gln Gln Gln
 350 275 280 285
 353 Val Leu Lys His Asn Gly Ser Ser Glu Ile Leu Asn Lys Leu Tyr Asp
 354 290 295 300
 357 Thr Ala Met Asp Lys Leu Glu Val Val Lys Lys Asp Tyr Asp Ala Leu
 358 305 310 315 320
 361 Arg Lys Arg Tyr Ser Glu Lys Val Ala Ile His Asn Ala Asp Leu Ser
 362 325 330 335
 365 Arg Leu Glu Gln Leu Gly Glu Glu Asn Gln Arg Leu Leu Lys Gln Thr
 366 340 345 350
 369 Glu Met Leu Thr Gln Gln Arg Asp Thr Ala Ile Gln Leu Gln His Gln
 370 355 360 365
 373 Cys Ala Leu Ser Leu Arg Arg Phe Glu Ala Ile His His Glu Leu Asn

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377	Lys Ala Thr Ala Gln Asn Lys Asp Leu Gln Trp Glu Met Glu Leu Leu		
378	385	390	395
381	Gln Ser Glu Leu Thr Glu Leu Arg Thr Thr Gln Val Lys Thr Ala Lys		400
382	405	410	415
385	Glu Ser Glu Lys Tyr Arg Glu Glu Arg Asp Ala Val Tyr Ser Glu Tyr		
386	420	425	430
389	Lys Leu Ile Met Ser Glu Arg Asp Gln Val Ile Ser Glu Leu Asp Lys		
390	435	440	445
393	Leu Gln Thr Glu Val Glu Leu Ala Glu Ser Lys Leu Lys Ser Ser Thr		
394	450	455	460
397	Ser Glu Lys Lys Ala Ala Asn Glu Glu Met Glu Ala Leu Arg Gln Ile		
398	465	470	475
401	480	485	490
402	Lys Asp Thr Val Thr Met Asp Ala Gly Arg Ala Asn Lys Glu Val Glu		495
405	Ile Leu Arg Lys Gln Cys Lys Ala Leu Cys Gln Glu Leu Lys Glu Ala		
406	500	505	510
409	Leu Gln Glu Ala Asp Val Ala Lys Cys Arg Arg Asp Trp Ala Phe Gln		
410	515	520	525
413	Glu Arg Asp Lys Ile Val Ala Glu Arg Asp Ser Ile Arg Thr Leu Cys		
414	530	535	540
417	Asp Asn Leu Arg Arg Glu Arg Asp Arg Ala Val Ser Glu Leu Ala Glu		
418	545	550	555
421	560	565	570
422	575	570	575
425	Arg Glu Leu Lys Glu Leu Lys Glu Gln Met Glu Ser Gln Leu Glu Lys		
426	580	585	590
429	590	595	600
430	605	600	605
433	Ile Asp Thr Asp Ser Met Glu Trp Glu Thr Glu Val Val Glu Phe Glu		
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437	620	625	630
438	635	630	640
441	640	645	650
442	655	650	655
445	660	665	670
446	670	675	680
449	680	685	685
450	690	695	700
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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date